UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/555,529	07/24/2000	PATRICIA KANNOUCHE	192863US0PCT	6934

			EXAMINER
22850	7590	03/06/2006	JOHANNSEN, DIANA B

OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
1940 DUKE STREET
ALEXANDRIA, VA 22314

ART UNIT	PAPER NUMBER
1634	

DATE MAILED: 03/06/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

PTO-90C (Rev. 10/03)

		Application No.	Applicant(s)
		09/555,529	KANNOUCHE ET AL.
Office Action Summary		Examiner	Art Unit
		Diana B. Johannsen	1634

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE <u>3</u> MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on <u>01 September 2005</u>.

2a)☒ This action is **FINAL**.   2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) <u>30-78</u> is/are pending in the application.

    4a) Of the above claim(s) <u>43-58,66-73 and 75-78</u> is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) <u>30-42,59-65 and 74</u> is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

    Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

    Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

    a)☐ All   b)☐ Some * c)☐ None of:

      1.☐ Certified copies of the priority documents have been received.

      2.☐ Certified copies of the priority documents have been received in Application No. _____.

      3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

    * See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1)☒ Notice of References Cited (PTO-892)

2)☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3)☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date <u>0203</u>.

4)☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .

5)☐ Notice of Informal Patent Application (PTO-152)

6)☒ Other: *sequence alignments*.

FINAL ACTION

1.   This action is responsive to the complying complete set of claims filed 01

September 2005, as well as to the Supplemental Response to Election of Species filed .

30 September 2003. Any rejections not reiterated in this action have been withdrawn.

This action is FINAL.

2.   It is noted that the new title and amendments to the specification filed 15 July

2004 (and re-submitted 01 September 2005) have been entered.

Election/Restriction

3.   It is again noted that the Amendment of 10 February 2003 canceled original

claims 1-29 (which claims were subject to the Restriction Requirement mailed 08 July

2002), and added new claims 30-78. New claims 30-42, 59-65, and 74-75 are drawn to

nucleic acids encoding proteins and fragments thereof, expression vectors, host cells,

and nucleic acid detection reagents, and therefore correspond to elected Group I.

4.   Newly submitted claims 43-58, 66-73, and 76-78 are directed to inventions that

are independent or distinct from the invention originally claimed and elected by

Applicant (see the Response to Restriction Requirement filed 08 August 2002) for the

following reasons:

-New claims 43-53, 66-73, and 76-78 are drawn to methods for detecting nucleic

acids, corresponding to non-elected Group II (original claims 6-12); and

-New claims 54-58 are drawn to methods in which polynucleotides are expressed

in cells so as to produce proteins that inhibit cell proliferation, corresponding to

non-elected Group VI (original claim 26).

Applicant has received an action on the merits for the originally presented and elected invention of Group I. As the inventions of claims 43-58, 66-73, and 76-78 correspond to non-elected inventions previously withdrawn from consideration, claims 43-58, 66-73, and 76-78 are also withdrawn from consideration as being directed to a non-elected invention. See 37 CFR 1.142(b) and MPEP § 821.03.

5.   Additionally, Applicant's election with traverse of SEQ ID Nos 18, 19, 27, and 28 in the reply filed on 06 June 2003 is acknowledged. The traversal is on the ground(s) that the Office "has not provided adequate reasons and/or examples to support a conclusion of patentable distinctness between the identified groups." The response continues that the statement by the examiner that "each primer pair is characterized by a different combination of particular nucleotide sequences and functions in the amplification of a different target sequence" is "an unsupported conclusion." This is not found persuasive because applicants' own specification provides the sequences of each primer (each of which differs from the other) and exemplifies the fact that each primer pair amplifies a different target sequence, such that the examiner's conclusion is supported by the teachings of applicants' own specification. Further, Applicants' response has provided no specific arguments supporting a conclusion different from that reached by the examiner (for example, applicants have not indicated what they believe might constitute a "special technical feature" shared by all the molecules encompassed by the claims). Accordingly, Applicants' arguments are not persuasive.

The requirement is still deemed proper and is therefore made FINAL.

It is noted that in the Supplemental Response of 30 September 2003, Applicant

clarified the fact that claims 45, 48, 49, 68, 71, 74, 76, and 77 read on the elected

primers. Of these claims, only claim 74 is encompassed by elected Group I.

Claim 75, which is encompassed by Group I, does not read on elected primers

SEQ ID NOS 18, 19, 27 and/or 28. Accordingly, claim 75 is withdrawn from further

consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention,

there being no allowable generic or linking claim. Applicant timely traversed the

restriction (election) requirement in the reply filed on 06 June 2003.

Claim 74 is also withdrawn from consideration to the extent that it is drawn to

non-elected sequences (i.e., sequences other than elected primers SEQ ID Nos 18-19

and a "fragment obtained by amplification of a kin17 nucleotide sequence with SEQ ID

NO: 18 and SEQ ID NO: 19").

6.   This application contains claims 43-58, 66-73, and 75-78 drawn to inventions

nonelected with traverse. A complete reply to the final rejection must include

cancellation of nonelected claims or other appropriate action (37 CFR 1.144). See

MPEP § 821.01.

7.   Applicants' request in the response of 10 February 2003 that non-elected

process claims be rejoined at such time as the elected claims are found allowable is

noted. However, no claims are allowed at this time.

Declaration under 37 CFR 1.132

8.   In view of the cancellation of original claims 1-5, 24-25 and 29, it is noted that the

rejections of those claims set forth in the Office action of 09 October 2002 are moot.

However, it is also noted that the Declaration under 37 CFR 1.132 filed 10 February

2003 is sufficient to disqualify the Kannouche et al reference (Biochimie 79:599-606

[1997]) as prior art under 35 USC 102(a).

Information Disclosure Statement

9.   The information disclosure statement filed 10 February 2003 fails to comply with

37 CFR 1.98(a)(2), which requires a legible copy of each cited foreign patent document;

each non-patent literature publication or that portion which caused it to be listed; and all

other information or that portion which caused it to be listed. Specifically, no copy of

reference AAA (M.D. Adams et al) has been provided; accordingly, that reference has

not been considered.

Claim Rejections - 35 USC § 112

10.   The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of
> making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the
> art to which it pertains, or with which it is most nearly connected, to make and use the same and shall
> set forth the best mode contemplated by the inventor of carrying out his invention.

THE FOLLOWING ARE NEW GROUNDS OF REJECTION NECESSITATED

BY APPLICANTS' AMENDMENTS TO THE CLAIMS

11.   Claims 39-42 and 64-65 are rejected under 35 U.S.C. 112, first paragraph, as

failing to comply with the written description requirement. The claim(s) contains subject

matter which was not described in the specification in such a way as to reasonably

convey to one skilled in the relevant art that the inventor(s), at the time the application

was filed, had possession of the claimed invention. This is a new matter rejection.

While applicants' specification discloses bacteria and particular lines of cells comprising vectors and plasmids that express various kin17 proteins and variants thereof (see, e.g., page 1 and examples throughout the specification), the specification as originally filed does not broadly disclose host cells comprising polynucleotides that encode such proteins, as encompassed by the instant claims. The specification does not refer to or provide any type of limiting definition of the term "host cell," and the claims as written are sufficiently broad so as to encompass any type of cell comprising the claimed polynucleotides in any form (including polynucleotides which are [unlike the molecules exemplified in the specification] free of any type of vector or plasmid construct). It is noted that Applicants have not provided any type of specific reference to locations in the specification that are believed to provide basis for the claims (rather, Applicants merely state that support is found "in Claims 1-29 and the specification as originally filed" (see the response of 10 February 2003)), and the examiner could not identify basis for this subject matter as it is now broadly claimed. Accordingly, claims 39-42 and 64-65 introduce new matter.

12.   The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

THE FOLLOWING ARE NEW GROUNDS OF REJECTION NECESSITATED BY APPLICANTS' AMENDMENTS TO THE CLAIMS

13.   Claims 30-42 and 59-65 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 30-42 and 49-65 are indefinite over the recitation of the language "kin17

protein which comprises an amino acid sequence wherein amino acids ___ to ___ are

deleted in SEQ ID NO:___" in claims 30, 32-34, and 59-60. This language does not

make clear the structural requirements of the molecules encompassed by the claims.

While the claims make reference to particular amino acids that are "deleted in" a SEQ

ID NO, the claims do not otherwise require that the "non-deleted" portion of that SEQ ID

NO be present in the claimed molecules. While one of skill in the art could clearly

identify a molecule comprising, e.g., the two portions of SEQ ID NO: 26 flanking a

particular "deleted" region, it is not clear how one would or could identify molecules

encompassed by the claims that do not include the "non-deleted" portion of the SEQ ID

NO referenced in the claims. Clarification is required.

Claim Rejections - 35 USC § 101

THE FOLLOWING ARE NEW GROUNDS OF REJECTION NECESSITATED BY

APPLICANTS' AMENDMENTS TO THE CLAIMS

14.   35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of
> matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the
> conditions and requirements of this title.

15.   Claims 39 and 65 are rejected under 35 U.S.C. 101 because the claimed

invention is directed to non-statutory subject matter. The claims do not sufficiently

distinguish over cells that exist naturally because the claims do not particularly point out

any non-naturally occurring differences between the claimed products and the naturally

occurring products. In the absence of the hand of man, the naturally occurring

products are considered non-statutory subject matter. *See Diamond v. Chakrabarty*, 447 U.S. 303, 206 USPQ 193 (1980).

Specifically, instant claims 39 and 65 as written encompass cells found in nature that comprise wild-type kin17 molecules. While it is noted that claims 31 and 61 (from which claims 39 and 65, respectively, depend) are drawn to "isolated" polynucleotides, as claims 39 and 65 are drawn to host cells that "comprise" such polynucleotides, the polynucleotides encompassed by claims 39 and 65 are not "isolated" molecules.

(With regard to claims 40-42 and 64 (which are also drawn to "host cells"), it is noted that as the host cells of these claims comprise deletion constructs that are not found in nature, these claims meet the requirements of 35 USC 101.)

Claim Rejections - 35 USC § 102

THE FOLLOWING ARE NEW GROUNDS OF REJECTION NECESSITATED BY APPLICANTS' AMENDMENTS TO THE CLAIMS

It is noted that while applicants' claims previously encompassed nucleic acid fragments of SEQ ID NO: 1 consisting of SEQ ID NO: 18 or SEQ ID NO: 19 (see, e.g., original claim 5), as well as a group of reagents including SEQ ID NO: 18 and SEQ ID NO: 19 (in combination with several other reagents; see, e.g., original claim 29), instant claim 74 encompasses both an isolated polynucleotide comprising SEQ ID NO: 18 and an isolated polynucleotide comprising SEQ ID NO: 19.

16.   The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

17.   Claim 74 is rejected under 35 U.S.C. 102(b) as being clearly anticipated by

Matsuda et al (The Journal of Biological Chemistry 268(33)24950-24958 [1993]).

Matsuda et al disclose double-stranded vectors comprising instant SEQ ID NO:

18 (see entire reference, particularly the "Materials and Methods" section at pages

24950 and Figure 3, particularly nucleotides –270 through –249, which are the reverse

complement of instant SEQ ID NO: 18). Accordingly, Matsuda et al clearly anticipate

the claimed invention.

18.   Claim 74 is rejected under 35 U.S.C. 102(a) as being clearly anticipated by EST

database accession no. AI089251 (NCI-CGAP; gb09a11.x1 Soares pregnant uterus

NbHPU Homo sapiens cDNA clone, 8/1998).

EST database accession no. AI089251 discloses a cDNA comprising instant

SEQ ID NO : 19 (see entire reference, particularly nucleotides 218-243 of the

sequence). Accordingly, EST database accession no. AI089251 clearly anticipates the

claimed invention.

Conclusion

19.   The prior art made of record and not relied upon is considered pertinent to

applicant's disclosure. Sequence alignments are provided to show the identity shared

between the nucleic acid of Matsuda et al and instant SEQ ID NO: 18, and the nucleic

acid of EST database accession no. AI089251 and instant SEQ ID NO: 19.

20.   Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Diana B. Johannsen whose telephone number is 571/272-0744. The examiner can normally be reached on Monday and Thursday, 7:30 am-4:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla can be reached at 571/272-0735. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the

Patent Application Information Retrieval (PAIR) system. Status information for

published applications may be obtained from either Private PAIR or Public PAIR.

Status information for unpublished applications is available through Private PAIR only.

For more information about the PAIR system, see http://pair-direct.uspto.gov. Should

you have questions on access to the Private PAIR system, contact the Electronic

Business Center (EBC) at 866-217-9197 (toll-free).

Diana B. Johannsen
Primary Examiner
Art Unit 1634   3/2/06

Sequence alignments

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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and is derived by analysis of the total score distribution.

SUMMARIES

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c 12	18.4	83.6	170597	5	AC146480	Danio rer
c 13	18.4	83.6	177953	2	AL929558	Zebrafish
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c 20	17.8	80.9	101798	14	AC150077	AC150077 Gallus ga
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c 26	17.4	79.1	3661	1	AR408798	AR408798 Sequence
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c 29	17.4	79.1	14663	1	D90744	D90744 Escherichia
c 30	17.4	79.1	103920	14	AC015817_3	Continuation (4 of
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c 40	17.2	78.2	412	6	CQ148085	CQ148085 Sequence
c 41	17.2	78.2	412	6	CQ183469	CQ183469 Sequence
c 42	17.2	78.2	412	6	CQ207864	CQ207864 Sequence
c 43	17.2	78.2	412	6	CQ231346	CQ231346 Sequence
c 44	17.2	78.2	412	6	CQ269518	CQ269518 Sequence
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ALIGNMENTS

RESULT 1
AX003325

LOCUS   AX003325   22 bp   DNA   linear   PAT 24-AUG-2000
DEFINITION   Sequence 18 from Patent WO9929845.
ACCESSION   AX003325
VERSION   AX003325.1 GI:9927142
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE   1
AUTHORS   Angulo-Mora,J.F. and Mauffrey,P.
TITLE   Sequences coding for kin17 protein and their applications
JOURNAL   Patent: WO 9929845-A 18 17-JUN-1999;
ANGULO MORA JAIME FRANCISCO (FR); COMMISSARIAT ENERGIE ATOMIQUE
(FR)
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ORIGIN

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Best Local Similarity 100.0%;
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Qy 1 AGAAAGTGATCGCTGCCGTGGT 22
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Db 1 AGAAAGTGATCGCTGCCGTGGT 22

RESULT 2
AX003310

LOCUS   AX003310   1002 bp   DNA   linear   PAT 24-AUG-2000
DEFINITION   Sequence 3 from Patent WO9929845.
ACCESSION   AX003310
VERSION   AX003310.1 GI:9927127
KEYWORDS .

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RESULT 6

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Db  40 AGAAAGTGATCGCTGCCGTGGT 61
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ACCESSION   D16561
VERSION   D16561.1 GI:468446
KEYWORDS   .
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            Hominidae; Homo.
REFERENCE   1 (bases 1 to 23065)
  AUTHORS   Matsuda,C., Endo,H., Ohta,S. and Kagawa,Y.
  TITLE   Gene structure of human mitochondrial ATP synthase gamma-subunit.
            Tissue specificity produced by alternative RNA splicing.
  JOURNAL   J. Biol. Chem. 268 (33), 24950-24958 (1993)
  PUBMED   8221057
REFERENCE   2 (bases 1 to 23065)
  AUTHORS   Kagawa,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (23-JUN-1993) Yasuo Kagawa, Jichi Medical School,
            Department of Biochemistry; 3311-1 Yakushiji, Minamikawachi-machi,
            Tochigi 329-0498, Japan (E-mail:ykagawa@ddb).n.ig.ac.jp,
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                     /protein_id="BAA03994.1"
                     /db_xref="GI:665584"
                     /translation="MFSRAGVAGLSAWTLQPQWIQVRNMATLKDITTRLKSIKNIQKI
                     TKSMKMVAAAKYARAERRLKPARIYGLGSLALYEKADIKGPEDKKHLLIGVSSDRGL
                     CGAIHSSIAKQMKSEVATLTAAGKEVMLVGIGDKIRGILYRTHSDQFLVAFKEVGRKP
                     PFGDASVIALELLNSGYEFDEGSIIFNKFRSVISLYKTEEKPIFSLNTVASADSMSIY
                     DDIDADVLQNYQEYNLANIIYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFN
                     RTRQAVTKELIEIISGAAAL"
     exon   4188..4274
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     intron   11204..12113
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     exon   12114..12245
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     exon   14057..14261
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     intron   14262..14838
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     exon   14839..14982
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                     /number=5
     exon   15094..15158
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     exon   17329..17484
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     intron   17485..17816
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     exon   17817..17913
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     intron   17914..22027
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     exon   22028..22064
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     intron   22065..22712
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     exon   22713..22869
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     polyA_signal   22835..22840
     polyA_signal   22849..22854
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                     /note="L(liver)-type ATP synthase gamma-subunit"
                     /codon_start=1
                     /product="ATP synthase gamma-subunit"
                     /protein_id="BAA03995.1"
                     /db_xref="GI:665583"
                     /translation="MFSRAGVAGLSAWTLQPQWIQVRNMATLKDITTRLKSIKNIQKI
                     TKSMKMVAAAKYARAERRLKPARIYGLGSLALYEKADIKGPEDKKHLLIGVSSDRGL
                     CGAIHSSIAKQMKSEVATLTAAGKEVMLVGIGDKIRGILYRTHSDQFLVAFKEVGRKP
                     DIDADVLQNYQEYNLANIIYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFN
                     RTRQAVTKELIEIISGAAALD"
     intron          4275..11168
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     exon            11169..11203
                     /number=2
     intron          11204..12113
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     exon            12114..12245
                     /number=3
     intron          12246..14056
                     /number=3
     exon            14057..14261
                     /number=4
     intron          14262..14838
                     /number=4
     exon            14839..14982
                     /number=5
     intron          14983..15093
                     /number=5
     exon            15094..15158
                     /number=6
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     intron          15159..17328
                     /number=6
     exon            17329..17484
                     /number=7
     intron          17485..17816
                     /number=7
     exon            17817..17913
                     /number=8
     intron          17914..22027
                     /number=8
     exon            22028..22064
                     /number=9
     intron          22065..22712
                     /number=9
     exon            22713..22869
                     /number=10
     polyA_signal    22835..22840
     polyA_signal    22849..22854
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RESULT 7

Query Match   100.0%;   Score 22;   DB 8;   Length 23065;
Best Local Similarity   100.0%;
Matches 22; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy     1 AGAAAGTGATCGCTGCCGTGGT 22
           ||||||||||||||||||||||
Db  3970 AGAAAGTGATCGCTGCCGTGGT 3949
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LOCUS   AL158044   174361 bp   DNA   linear   PRI 18-MAY-2005
DEFINITION Human DNA sequence from clone RP11-264C14 on chromosome 10 Contains
            the 5' end of the gene for a novel protein (MGC10848), the ITIH2
            gene for inter-alpha (globulin) inhibitor, H2 polypeptide (H2P),
            the KIN gene for KIN, antigenic determinant of recA protein homolog
            (mouse), the 3' end of the ATP5C1 gene for ATP synthase, H+
            transporting, mitochondrial F1 complex, gamma polypeptide 1
            (ATP5C1,ATP5C1i), a novel gene and two CpG islands, complete
            sequence.
ACCESSION   AL158044

OM nucleic - nucleic search, using sw model

Run on: November 26, 2005, 12:58:53 ; Search time 145.336 Seconds
(without alignments)
8370.011 Million cell updates/sec

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Title: US-09-555-529-19
Perfect score: 26
Sequence: 1 gcgaacaccaattgatgcttaaga 26

Scoring table: IDENTITY_NUC
Scoring: Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 2339541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : EST:*
    1: gb_est1:*
    2: gb_est2:*
    3: gb_est3:*
    4: gb_htc:*
    5: gb_est4:*
    6: gb_est5:*
    7: gb_est6:*
    8: gb_est7:*
    9: gb_gss1:*
   10: gb_gss2:*
   11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Match	Query Length	Match DB	DB ID	Description
1		26	100.0	249	1	AI493544	AI493544 th36a10.x
2		26	100.0	328	2	BE091046	BE091046 PM4-BT072
3		26	100.0	384	1	AA770446	AA770446 ah89e07.s
4		26	100.0	384	1	AI493563	AI493563 th36c10.x
5		26	100.0	386	1	BM661987	BM661987 UI-E-CK1-
6		26	100.0	469	1	AI087818	AI087818 oo24o09.x
7		26	100.0	476	1	AI378396	AI378396 tc78f05.x
8		26	100.0	485	3	AI089251	AI089251 qb09a11.x
9		26	100.0	488	3	BM689918	BM689918 UI-E-CK1-
10		26	100.0	512	5	BQ548883	BQ548883 ik93a03.y
11		26	100.0	516	2	BG944189	BG944189 ax47e12.x
12		26	100.0	521	2	BE349628	BE349628 ht58g10.x
13		26	100.0	543	6	CB158644	CB158644 K-EST0218
14		26	100.0	591	2	BM750112	BM750112 K-EST0025
15		26	100.0	591	2	BB896845	BB896845 60143754B
16		26	100.0	592	8	CX866354	CX866354 HBSC4_10
17		26	100.0	605	6	CB242699	CB242699 UI-CF-FN0
18		26	100.0	660	5	AL597250	AL597250 DKFZp313A
19		26	100.0	682	1	AV721396	AV721396 AV721396
20		26	100.0	698	1	AI650375	AI650375 wa90b01.x
21		26	100.0	701	1	AI807250	AI807250 wf38f05.x
22		26	100.0	720	7	CK301009	CK301009 UI-E-EJ1-
23	c	26	100.0	733	5	BX104466	BX104466 BX104466
24	c	26	100.0	848	1	AL558810	AL558810 AL558810
25	c	26	100.0	1339	4	CR618602	CR618602 full-leng
26	c	26	100.0	1396	4	CR595908	CR595908 full-leng
27	c	25	96.2	723	3	BQ186497	BQ186497 UI-E-EJ1-
28	c	24.4	93.8	259	6	CF526711	CF526711 tu-t-c-14
29	c	24.4	93.8	349	1	AA805923	AA805923 oc13d08.s
30	c	24.4	93.8	558	5	BU737321	BU737321 UI-E-DX1-
31	c	24.4	93.8	679	1	AM028238	AM028238
32	c	24.4	93.8	691	1	AM028686	AM028686
33	c	24.4	93.8	703	1	AM035210	AM035210
34	c	24.4	93.8	776	2	BF571691	BF571691 602075248
35	c	24.4	93.8	786	1	AJ819816	AJ819816
36	c	24.4	93.8	864	1	AM037867	AM037867
37	c	24.4	93.8	871	1	AJ819723	AJ819723
38	c	24.4	93.8	949	3	BM453332	BM453332 AGENCOURT
39	c	23	88.5	477	1	AJ656645	AJ656645
40	c	23	88.5	624	5	BQ602324	BQ602324 MI-P-HO-a
41	c	23	88.5	663	1	AJ660240	AJ660240 MI-P-HO-a
42	c	23	88.5	682	5	CF995929	CF995929 892135 MA
43	c	23	88.5	1543	4	AY609991	AY609991 Sus scrof
44	c	22.8	87.7	800	1	AM038283	AM038283
45	c	22	84.6	398	8	H75516	H75516 yu58e09.r1

ALIGNMENTS

RESULT 1
AI493544
AI493544 th36a10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120346 3',
mRNA sequence.

LOCUS   AI493544   249 bp   mRNA   linear   EST 30-MAR-1999
DEFINITION AI493544 th36a10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone
            IMAGE:2120346 3', mRNA sequence.
ACCESSION   AI493544
VERSION   AI493544.1 GI:4394547
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 249)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap)
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Life Technologies catalog #: 11548-013
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www.bio.llnl.gov/bbrp/image/image.html
            Insert Length: 841   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 246.
FEATURES   Location/Qualifiers
     source   1..249
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2120346"
                     /tissue_type="adenocarcinoma"
                     /clone_lib="NCI_CGAP_Pan1"
                     /lab_host="DH10B"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
                     Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.72 kb. Life Technologies catalog #:
                     11548-013"
ORIGIN

Query Match   100.0%; Score 26; DB 1; Length 249;
Best Local Similarity   100.0%;

RESULT 7
LOCUS   AI378396   476 bp   mRNA   linear   EST 18-MAR-1999
DEFINITION   tc78f05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:2070753
               3', mRNA sequence.
ACCESSION   AI378396
VERSION   AI378396.1 GI:4188249
KEYWORDS   EST.
SOURCE   Homo sapiens
ORGANISM   Homo sapiens (human)
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE   1 (bases 1 to 476)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               This clone is available royalty-free through LLNL ; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               Seq primer: -40UP from Gibco
               High quality sequence stop: 442.
               Insert Length: 625   Std Error: 0.00
FEATURES   Location/Qualifiers
     source   1..476
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2070753"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /clone_lib="Soares_NhHMPu_S1"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."

ORIGIN

Query Match   100.0%; Score 26; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

              1 GCGAACACCAATTTGATGCTTTAAGA 26

RESULT 8
Db   AI089251

                     ||||||||||||||||||||||||||
          218 GCGAACACCAATTTGATGCTTTAAGA 243

LOCUS   AI089251   485 bp   mRNA   linear   EST 18-AUG-1998
DEFINITION   qb09all.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone
               IMAGE:1695740 3', mRNA sequence.
ACCESSION   AI089251
VERSION   AI089251.1 GI:3428310
KEYWORDS   EST.
SOURCE   Homo sapiens
ORGANISM   Homo sapiens (human)
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE   1 (bases 1 to 485)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               This clone is available royalty-free through LLNL ; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               Seq primer: -40m13 fwd. ET from Amersham
               High quality sequence stop: 442.
FEATURES   Location/Qualifiers
     source   1..485
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1695740"
                     /sex="female"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="Soares_pregnant_uterus_NbHPU"
                     /note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
                     Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
                     oligo(dT) primer [5'-
                     AACTGGAAGAATTCGCGGCCGCCCTTTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization. Library
                     constructed by M. Fatima Bonaldo."

ORIGIN

Query Match   100.0%; Score 26; DB 1; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 26; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GCGAACACCAATTTGATGCTTTAAGA 26
                ||||||||||||||||||||||||||
Db   218 GCGAACACCAATTTGATGCTTTAAGA 243

RESULT 9
BM689918/c
LOCUS   BM689918   488 bp   mRNA   linear   EST 28-FEB-2002
DEFINITION   UI-E-CK1-abo-f-09-0-UI.r1 UI-E-CK1 Homo sapiens cDNA clone
               UI-E-CK1-abo-f-09-0-UI 5', mRNA sequence.
ACCESSION   BM689918
VERSION   BM689918.1 GI:19003176
KEYWORDS   EST.
SOURCE   Homo sapiens
ORGANISM   Homo sapiens (human)
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE   1 (bases 1 to 488)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.